AMENDMENTS TO THE CLAIMS

1. – 39. (Canceled)

40. (Withdrawn) A method of making a polypeptide comprising expressing the sequence corresponding to the open reading frame of a polynucleotide according to Claim 57.

41. (Previously Presented) A diagnostic reagent for the differential detection of a human endogenous retroviral sequence comprising a polynucleotide having a sequence ~~is~~ selected from the group consisting of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22, a sequence complementary to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22.

42. (Previously Presented) The diagnostic reagent according to Claim 41, wherein said polynucleotide further comprises a label for detection.

43. (Previously Presented) The diagnostic reagent according to Claim 41, wherein said polynucleotide is selected from the group consisting of nucleotides 3065-4390 of SEQ ID NO: 3, nucleotides 6965-9550 of SEQ ID NO: 3, and nucleotides 2502-2865 of SEQ ID NO: 3.

44. – 45. (Canceled)

46. (Withdrawn) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) contacting a biological sample with at least one diagnostic reagent comprising one or more polynucleotides according to Claim 57, and

(b) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

47. (Withdrawn) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) preparing a biological tissue or fluid,

(b) extracting a nucleic acid to be detected,

(c) contacting the nucleic acid with at least one diagnostic reagent comprising one or more polynucleotides according to Claim 57,

(d) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

(e) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22.

48. (Withdrawn) The method according to Claim 47, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

49. (Withdrawn) A method of detecting a polypeptide encoded by a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, comprising:

collecting messenger RNAs obtained from a control biological sample and from a sample collected from patient, and

analyzing qualitatively and/or quantitatively said mRNAs using ~~the~~ a diagnostic ~~aid~~ reagent comprising one or more polynucleotides according to Claim 57 by a technique selected from the group consisting of *in situ* hybridization, by dot-blot, Northern blotting, RNAse mapping and RT-PCR.

50. (Withdrawn) A recombinant cloning or expression vector comprising the polynucleotide according to Claim 57.

51. (Withdrawn) A method of making a diagnostic reagent comprising mixing the polynucleotide according to Claim 57 with a suitable medium.

52. (Withdrawn) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to Claim 57 with a suitable medium,

(b) contacting a biological sample with said diagnostic reagent, and

(c) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

53. (Withdrawn) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to Claim 57 with a suitable medium,

(b) preparing a biological tissue or fluid,

(c) extracting a nucleic acid to be detected,

(d) contacting the nucleic acid with said diagnostic reagent,

(e) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

(f) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: 1, 2, 3-8, 10, 13, 16, 17, and 22.

54. (Withdrawn) The method according to Claim 53, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

55. (Withdrawn) A method of making a detection kit, comprising mixing one or more polynucleotides according to Claim 57 with at least one reagent selected from the group consisting of the transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/de regulation or alteration is associated with the normal or pathological expression or with the regulation/deregulation of motifs belonging to said HERV-7q family, these sequences corresponding to nucleotide sequences encoding genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of said HERV-7q family, of which one of the ends cannot be at a distance exceeding 120 kb.

56. (Withdrawn) The method according to Claim 55, further comprising attaching said polynucleotide and said reagents to a support.

57. (Currently Amended) A purified polynucleotide consisting of a polynucleotide sequence selected from the group consisting of:

a) a sequence selected from the group consisting of SEQ ID NO: 3-8, 10, 13, 16, 17, 20, 21, and 22;

b) a complementary sequence to the sequence of a);

c) a reverse complementary sequence to the sequence of a) or b);

d) a fragment ~~derived from the~~ of a coding region of the sequence of a), wherein said fragment corresponds to a coding frame of at least 14 nucleotides; and

a complementary sequence to the sequence of d).

58. (Previously Presented) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of SEQ ID NO: 1 or SEQ ID NO: 2.

59. (Currently Amended) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of a sequence encoding the C-terminal portion of enverin ~~from amino acid 291 from the first methionine,~~ wherein said sequence ~~starting from~~ begins at the codon at positions 8749 to 8751 of SEQ ID NO: 3 and contains at least 14 nucleotides.

60. (Currently Amended) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of a sequence encoding the C-terminal portion of enverin ~~from amino acid 321 from the first methionine,~~ wherein said sequence ~~starting from~~ begins at the codon at positions 8839 to 8841 of SEQ ID NO: 3 and contains at least 14 nucleotides.

## BASIS FOR THE AMENDMENT

Claims 1-39, 44, and 45 were previously canceled.

Claims 57, 59, and 60 have been amended.

The amendment of Claims 57, 59, and 60 are supported by the claims as previously presented, as well as the specification and Sequence Listing as originally filed.

No new matter is added by the present amendment.